Patent claims

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the lysR2 gene, chosen from the group consisting of

a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least to [sic] 70% to the amino acid sequence of SEQ ID No. 2,

c) polynucleotide which is complementary to the polynucleotides of a) or b), and

d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b), or c),

the polypeptide preferably having the activity of the transcription regulator LysR2.

2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.

3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

4. A DNA as claimed in claim 2 which is capable of replication, comprising

(i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequences complementary to sequences (i) or (ii), and optionally

(iv) (iv)[sic] sense mutations of neutral function in (i) which do not modify the activity of the protein/polypeptide.

5. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

6. The vector pCR2.1lysR2int, which

6.1 carries an internal fragment of the citA gene 439 bp in size,

6.2 the restriction map of which is reproduced in figure 1, and

6.3 which is deposited in the E.coli strain TOP10F/pCR2.1lysR2int under no. DSM 13617 at the Deutsche Sammlung für Mikroorganismen und Zellenkulturen [German Collection of Microorganisms and Cell Cultures].

7. A coryneform bacterium in which the lysR2 gene is attenuated, preferably eliminated, in particular by deletion.

8. A process for the preparation of L-amino acids, in particular L-lysine and L-valine, which comprises carrying out the following steps,

a) fermentation of the bacteria which produce the desired L-amino acid and in which at least the lysR2 gene is attenuated,

b) concentration of the desired product in the medium or in the cells of the bacteria and

c) isolation of the L-amino acid.

9. A process as claimed in claim 8, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

10. A process as claimed in claim 8, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

11. A process as claimed in claim 8, wherein expression of the polynucleotide(s) which codes (code) for the lysR2 gene is decreased, in particular eliminated.

12. A process as claimed in claim 8, wherein the regulatory properties of the polypeptide for which the polynucleotide lysR2 codes are decreased.

13. A process as claimed in claim 8, wherein for the preparation of L-amino acids, in particular L-lysine, bacteria in which at the same time one or more of the genes chosen from the group consisting of

13.1 the dapA gene which codes for dihydrodipicolinate synthase,

13.2 the eno gene which codes for enolase,

13.3 the zwf gene which codes for the zwf gene product,

13.4 the pyc gene which codes for pyruvate carboxylase,

13.5 the lysE gene which codes for lysine export,

13.6 the lysC gene which codes for a feed-back resistant aspartate kinase

13.7 the zwa1 gene which codes for the Zwa1 protein

is or are enhanced, preferably over-expressed, are fermented.

14. A process as claim in claim 8, wherein
at the same time one or more of the genes chosen from the group consisting of:

14.1 the pck gene which codes for phosphoenol pyruvate carboxykinase,

14.2 the pgi gene which codes for glucose 6-phosphate isomerase,

14.3 the poxB gene which codes for pyruvate oxidase,

14.4 the zwa2 gene which codes for the Zwa2 protein,

14.5 the hom gene which codes for homoserine dehydrogenase

14.6 the thrB gene which codes for homoserine kinase, and

14.7 the panD gene which codes for aspartate decarboxylase

is or are attenuated, in particular eliminated.

15. A process as claimed in claim 8, wherein for the preparation of L-amino acids, in particular L-valine, bacteria in which at the same time one or more of the genes chosen from the group consisting of

15.1 the ilvBN gene which codes for acetohydroxy-acid synthase,

15.2 the ilvD gene which codes for dihydroxy-acid dehydratase,

15.3 the mqo gene which codes for malate:quinone oxidoreductase

is or are enhanced, in particular over-expressed, are fermented.

16. A process as claimed in one or more of the preceding claims, wherein microorganisms of the species Corynebacterium glutamicum or Brevibacterium lactofermentum are employed.

17. A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for the transcription regulator LysR2 or have a high similarity with the sequence of the lysR2 gene, which comprises employing the polynucleotide sequences as claimed in claims 1 to 4 as hybridization probes.

18. A process as claimed in claim 15, wherein arrays, micro arrays or DNA chips are employed.